

SEQUENCE LISTING

<110> Wu, Hongjiang
Crooke, Stanley T.

<120> Human RNase III And Compostions And Uses Thereof

<130> ISIS5029/ISPH-0522

<140> 09/900,425

<141> 2001-07-06

<160> 37

<170> PatentIn version 3.1

<210> 1

<211> 4764

<212> DNA

<213> Homo sapiens

<400> 1

```

ctgtcttggg acctgcggta gtagcctggc tttgctctga cggcgatctc gcggcccagag      60
agccttttat aggttgcttt tcccggggat gtgaaggata cagaaatgac tgtgaatcaa      120
cccatatcat caaggagctg ataatctagt ggaagagtta gacgtgtgca tacttcacta      180
tgatatgagg cagtctctga gcttatattc tctgtggaag atgtgacata tccaggcgga      240
acatcatgat gcagggaaac acatgtcaca gaatgtcgtt ccacccggga cgagggcgtc      300
cccgaggacg aggaggacat ggagccagac cctcagcacc atcctttagg ccccaaaatc      360
tgaggctgct tcaccctcag cagcctcctg tgcaatatca atatgaacct ccaagtgcc      420
cttcaccac tttctcaaac totccagccc ccaattttct ccctccacga ccagactttg      480
tacccttccc cccacccatg cctccgtcag cgcaaggccc tcttcccccc tgcccaatca      540
ggccgccttt cccaaccac cagatgaggc accccttccc agttcctcct tgttttctc      600
ccatgccacc accaatgcct tgtcctaata accccccagt ccctggggca cctcctggac      660
aaggcacttt ccccttcatg atgccccctc cctccatgcc tcatcccccg cccctccag      720
tcatgccgca gcaggttaat tatcagtacc ctccgggcta ttctcaccac aacttccac      780
ctcccagttt taatagtttc cagaacaacc ctagttcttt cctgccagat gctaataaca      840
gcagtagtcc tcatttcaga catctccctc catacccact cccaaaggct cccagtgaga      900
gaaggtcccc agaaaggctg aaacactatg atgaccacag gcaccgagac cacagtcag      960
ggcgagggtga gaggcatcgg tccctggatc ggcgggagcg aggccgcagt cccgacagga     1020

```

gaagacaaga cagccggtac agatctgatt atgaccgagg gagaacacca tctcgccacc 1080
 gcagctacga acggagcaga gagcgagaac gggagagaca caggcatcga gacaaccgaa 1140
 gatcaccatc tctggaaagg tcctacaaaa aagagtataa gagatctgga aggagttacg 1200
 gtttatcggg tggtcctgaa cctgctggat gcacaccaga attacctggg gagattatta 1260
 aaaatacaga ttcttgggcc ccaccctgg agattgtgaa tcatcgctcc ccaagtaggg 1320
 agaagaagag agctcgttgg gaggaagaaa aagaccgttg gaggtagaac cagagttctg 1380
 gcaaagacaa gaactatacc tcaatcaagg aaaaagagcc cgaggagacc atgcctgaca 1440
 agaatgagga ggaagaagaa gaacttctta agcctgtgtg gattcgatgc actcattcag 1500
 aaaactacta ctccagtgc cccatggatc aggtgggaga ttctacagtg gttggaacga 1560
 gtaggcttcg tgacttatat gacaaatttg aggaggagtt ggggagcagg caagaaaagg 1620
 ccaaagctgc tgggctccg tgggaacctc caaagacgaa gctcgatgaa gatttagaga 1680
 gttccagtga atccgagtgt gagtctgatg aggacagcac ctgttctagc agtcagact 1740
 ctgaagtttt tgacgttatt gcagaaatca aacgcaaaaa ggcccacct gaccgacttc 1800
 atgatgaact ttggtacaac gatccaggcc agatgaatga tggaccactc tgcaaagca 1860
 gcgcaaaggc aagacgcaca ggaattaggc acagcattta tcctggagaa gaggccatca 1920
 agccctgtcg tcctatgacc aacaatgctg gcagactttt ccactaccgg atcacagtct 1980
 ccccgccctac gaacttttta actgacaggc caactgttat agaatacgat gatcacgagt 2040
 atatctttga aggattttct atgtttgcac atgccccct gaccaatatt ccactgtgta 2100
 aagtaattag attcaacata gactacacga ttcatttcat tgaagagatg atgccggaga 2160
 atttttgtgt gaaagggctt gaactctttt cactgttctt attcagagat attttggaat 2220
 tatatgactg gaatcttaaa ggtcctttgt ttgaagacag ccctccctgc tgccaagat 2280
 ttcatttcat gccacgtttt gtaagatttc ttccagatgg aggaaaggaa gtgctgtcca 2340
 tgcaccagat tctcctgtac ttgttaaggc gcagcaaagc cctgggtgcct gaggaggaga 2400
 ttgccaatat gcttcagtgg gaggagctgg agtggcagaa atatgcagaa gaatgcaaag 2460
 gcatgattgt taccaacctc gggacgaaac caagctctgt ccgtatcgat caactggatc 2520
 gtgaacagtt caaccccgat gtgattactt ttccgattat cgtccacttt gggatacgcc 2580
 ctgcacagtt gagttatgca ggagacccac agtacaaaa actgtggaag agttatgtga 2640
 aacttcgcca cctcctagca aatagtccca aagtcaaaca aactgacaaa cagaagctgg 2700
 cacagagggg ggaagccctc caaaaaatac ggcagaagaa tacaatgaga cgagaagtaa 2760

cggtggagct aagtagccaa ggattctgga aaactggcat ccgttctgat gtctgtcagc	2820
atgcaatgat gctacctgtt ctgacccatc atatccgcta ccaccaatgc ctaatgcatt	2880
tggaacaagt gataggatat actttccaag atcgttgtct gttgcagctg gccatgactc	2940
atccaagtca tcatttaaatt tttggaatga atcctgatca tgccaggaat tcattatcta	3000
actgtggaat tcggcagccc aaatacggag acagaaaagt tcatcacatg cacatgcgga	3060
agaaagggat taacaccttg ataaatatca tgtcacgcct tggccaagat gacccaactc	3120
cctcgaggat taaccacaat gaacggtttg aattcctggg tgatgctgtt gttgaatttc	3180
tgaccagcgt ccatttgtac tatttgtttc ctagtctgga agaaggagga ttagcaacct	3240
atcggactgc cattgttcag aatcagcacc ttgccatgct agcaaagaaa cttgaactgg	3300
atccatttat gctgtatgct cacgggcctg acctttgtag agaatcggac cttcgacatg	3360
caatggccaa ttgttttgaa gcgttaatag gagctgttta cttggaggga agcctggagg	3420
aagccaagca gttatttgga cgcttgctct ttaatgatcc ggacctgcgc gaagtctggc	3480
tcaattatcc tctccacca ctccaactac aagagccaaa tactgatcga caacttattg	3540
aaacttctcc agttctacaa aaacttactg agtttgaaga agcaattgga gtaattttta	3600
ctcatgttcg acttctggca agggcattca cattgagaac tgtgggattt aaccatctga	3660
ccctaggcca caatcagaga atggaattcc taggtgactc cataatgcaa ctggtagcca	3720
cagagtactt attcattcat ttcccagatc atcatgaagg aacttaact ttgttgcgaa	3780
gctctttggt gaataataga actcaggcca aggtagcgga ggagctgggc atgcaggagt	3840
acgccataac caacgacaag accaagaggc ctgtggcgct tcgcaccaag accttggcgg	3900
accttttggga atcatttatt gcagcgctgt aactgataa ggatttggaa tatgttcata	3960
ctttcatgaa tgtctgcttc ttccacgat tgaaagaatt cttttgaat caggattgga	4020
atgaccccaa atcccagctt cagcagtgtt gcttgacact taggacagaa ggaaaagagc	4080
cagacattcc tctgtacaag actctgcaga cagtgggccc atcccatgcc cgaacctaca	4140
ctgtggctgt ttatttcaag ggagaaagaa taggctgtgg gaaaggacca agtattcagc	4200
aagcggaaat gggagcagca atggatgcgc ttgaaaaata taattttccc cagatggccc	4260
atcagaagcg gttcatcgaa cggaagtaca gacaagagtt aaaagaaatg aggtgggaaa	4320
gagagcatca agagagagag ccagatgaga ctgaagacat caagaaataa aggagggcat	4380
gcaagtgtgg agtatttact tgctcagtaa ctgtgactgt tgtctattga gacctagcct	4440

agttttcctg cagacaatga acgaagtgtg ctcattgaaa taaaatacag agtcaaatacg 4500
ctattgttgt tttaatgatc tgtttttagc tggatgggtct ttattacaaa gtattagatt 4560
tttcttctat ttaacggaaa acttgacttt ggtgaatgtg cattacttcc ttttattttg 4620
ctcttttaaat aataaaaattc aagaagcata ttctatgtgg aatagatcct gtttttccat 4680
ctgtgtccca gattgtgacc ctagactttc aattgacaag taaaaaattg actttactag 4740
taaaaaaaaa aaaaaaaaaa aaaa 4764

<210> 2
<211> 1374
<212> PRT
<213> Homo sapiens

<400> 2

Met Met Gln Gly Asn Thr Cys His Arg Met Ser Phe His Pro Gly Arg
1 5 10 15

Gly Cys Pro Arg Gly Arg Gly Gly His Gly Ala Arg Pro Ser Ala Pro
20 25 30

Ser Phe Arg Pro Gln Asn Leu Arg Leu Leu His Pro Gln Gln Pro Pro
35 40 45

Val Gln Tyr Gln Tyr Glu Pro Pro Ser Ala Pro Ser Thr Thr Phe Ser
50 55 60

Asn Ser Pro Ala Pro Asn Phe Leu Pro Pro Arg Pro Asp Phe Val Pro
65 70 75 80

Phe Pro Pro Pro Met Pro Pro Ser Ala Gln Gly Pro Leu Pro Pro Cys
85 90 95

Pro Ile Arg Pro Pro Phe Pro Asn His Gln Met Arg His Pro Phe Pro
100 105 110

Val Pro Pro Cys Phe Pro Pro Met Pro Pro Pro Met Pro Cys Pro Asn
115 120 125

Asn Pro Pro Val Pro Gly Ala Pro Pro Gly Gln Gly Thr Phe Pro Phe
130 135 140

Met Met Pro Pro Pro Ser Met Pro His Pro Pro Pro Pro Val Met

145

150

155

160

Pro Gln Gln Val Asn Tyr Gln Tyr Pro Pro Gly Tyr Ser His His Asn
165 170 175

Phe Pro Pro Pro Ser Phe Asn Ser Phe Gln Asn Asn Pro Ser Ser Phe
180 185 190

Leu Pro Ser Ala Asn Asn Ser Ser Ser Pro His Phe Arg His Leu Pro
195 200 205

Pro Tyr Pro Leu Pro Lys Ala Pro Ser Glu Arg Arg Ser Pro Glu Arg
210 215 220

Leu Lys His Tyr Asp Asp His Arg His Arg Asp His Ser His Gly Arg
225 230 235 240

Gly Glu Arg His Arg Ser Leu Asp Arg Arg Glu Arg Gly Arg Ser Pro
245 250 255

Asp Arg Arg Arg Gln Asp Ser Arg Tyr Arg Ser Asp Tyr Asp Arg Gly
260 265 270

Arg Thr Pro Ser Arg His Arg Ser Tyr Glu Arg Ser Arg Glu Arg Glu
275 280 285

Arg Glu Arg His Arg His Arg Asp Asn Arg Arg Ser Pro Ser Leu Glu
290 295 300

Arg Ser Tyr Lys Lys Glu Tyr Lys Arg Ser Gly Arg Ser Tyr Gly Leu
305 310 315 320

Ser Val Val Pro Glu Pro Ala Gly Cys Thr Pro Glu Leu Pro Gly Glu
325 330 335

Ile Ile Lys Asn Thr Asp Ser Trp Ala Pro Pro Leu Glu Ile Val Asn
340 345 350

His Arg Ser Pro Ser Arg Glu Lys Lys Arg Ala Arg Trp Glu Glu Glu
355 360 365

Lys Asp Arg Trp Ser Asp Asn Gln Ser Ser Gly Lys Asp Lys Asn Tyr
370 375 380

Thr Ser Ile Lys Glu Lys Glu Pro Glu Glu Thr Met Pro Asp Lys Asn
385 390 395 400

Glu Glu Glu Glu Glu Glu Leu Leu Lys Pro Val Trp Ile Arg Cys Thr
405 410 415

His Ser Glu Asn Tyr Tyr Ser Ser Asp Pro Met Asp Gln Val Gly Asp
420 425 430

Ser Thr Val Val Gly Thr Ser Arg Leu Arg Asp Leu Tyr Asp Lys Phe
435 440 445

Glu Glu Glu Leu Gly Ser Arg Gln Glu Lys Ala Lys Ala Ala Arg Pro
450 455 460

Pro Trp Glu Pro Pro Lys Thr Lys Leu Asp Glu Asp Leu Glu Ser Ser
465 470 475 480

Ser Glu Ser Glu Cys Glu Ser Asp Glu Asp Ser Thr Cys Ser Ser Ser
485 490 495

Ser Asp Ser Glu Val Phe Asp Val Ile Ala Glu Ile Lys Arg Lys Lys
500 505 510

Ala His Pro Asp Arg Leu His Asp Glu Leu Trp Tyr Asn Asp Pro Gly
515 520 525

Gln Met Asn Asp Gly Pro Leu Cys Lys Cys Ser Ala Lys Ala Arg Arg
530 535 540

Thr Gly Ile Arg His Ser Ile Tyr Pro Gly Glu Glu Ala Ile Lys Pro
545 550 555 560

Cys Arg Pro Met Thr Asn Asn Ala Gly Arg Leu Phe His Tyr Arg Ile
565 570 575

Thr Val Ser Pro Pro Thr Asn Phe Leu Thr Asp Arg Pro Thr Val Ile
580 585 590

Glu Tyr Asp Asp His Glu Tyr Ile Phe Glu Gly Phe Ser Met Phe Ala
595 600 605

His Ala Pro Leu Thr Asn Ile Pro Leu Cys Lys Val Ile Arg Phe Asn
610 615 620

Ile Asp Tyr Thr Ile His Phe Ile Glu Glu Met Met Pro Glu Asn Phe
625 630 635 640

Cys Val Lys Gly Leu Glu Leu Phe Ser Leu Phe Leu Phe Arg Asp Ile
645 650 655

Leu Glu Leu Tyr Asp Trp Asn Leu Lys Gly Pro Leu Phe Glu Asp Ser
660 665 670

Pro Pro Cys Cys Pro Arg Phe His Phe Met Pro Arg Phe Val Arg Phe
675 680 685

Leu Pro Asp Gly Gly Lys Glu Val Leu Ser Met His Gln Ile Leu Leu
690 695 700

Tyr Leu Leu Arg Cys Ser Lys Ala Leu Val Pro Glu Glu Glu Ile Ala
705 710 715 720

Asn Met Leu Gln Trp Glu Glu Leu Glu Trp Gln Lys Tyr Ala Glu Glu
725 730 735

Cys Lys Gly Met Ile Val Thr Asn Pro Gly Thr Lys Pro Ser Ser Val
740 745 750

Arg Ile Asp Gln Leu Asp Arg Glu Gln Phe Asn Pro Asp Val Ile Thr
755 760 765

Phe Pro Ile Ile Val His Phe Gly Ile Arg Pro Ala Gln Leu Ser Tyr
770 775 780

Ala Gly Asp Pro Gln Tyr Gln Lys Leu Trp Lys Ser Tyr Val Lys Leu
785 790 795 800

Arg His Leu Leu Ala Asn Ser Pro Lys Val Lys Gln Thr Asp Lys Gln
805 810 815

Lys Leu Ala Gln Arg Glu Glu Ala Leu Gln Lys Ile Arg Gln Lys Asn
820 825 830

Thr Met Arg Arg Glu Val Thr Val Glu Leu Ser Ser Gln Gly Phe Trp
835 840 845

Lys Thr Gly Ile Arg Ser Asp Val Cys Gln His Ala Met Met Leu Pro
850 855 860

Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu Met His Leu Asp
865 870 875 880

Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu Leu Gln Leu Ala
885 890 895

Met Thr His Pro Ser His His Leu Asn Phe Gly Met Asn Pro Asp His
900 905 910

Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln Pro Lys Tyr Gly
915 920 925

Asp Arg Lys Val His His Met His Met Arg Lys Lys Gly Ile Asn Thr
930 935 940

Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp Pro Thr Pro Ser
945 950 955 960

Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Val
965 970 975

Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro Ser Leu Glu
980 985 990

Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val Gln Asn Gln His
995 1000 1005

Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro Phe Met Leu Tyr
1010 1015 1020

Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu Arg His Ala Met
1025 1030 1035 1040

Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr Leu Glu Gly Ser
1045 1050 1055

Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu Phe Asn Asp Pro

1060

1065

1070

Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His Pro Leu Gln Leu
 1075 1080 1085

Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr Ser Pro Val Leu
 1090 1095 1100

Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val Ile Phe Thr His
 1105 1110 1115 1120

Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr Val Gly Phe Asn
 1125 1130 1135

His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe Leu Gly Asp Ser
 1140 1145 1150

Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile His Phe Pro Asp
 1155 1160 1165

His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser Leu Val Asn Asn
 1170 1175 1180

Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met Gln Glu Tyr Ala
 1185 1190 1195 1200

Ile Thr Asn Asp Lys Thr Lys Arg Pro Val Gly Leu Arg Thr Lys Thr
 1205 1210 1215

Leu Ala Asp Leu Leu Glu Ser Phe Ile Ala Ala Leu Tyr Thr Asp Lys
 1220 1225 1230

Asp Leu Glu Tyr Val His Thr Phe Met Asn Val Cys Phe Phe Pro Arg
 1235 1240 1245

Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Asp Pro Lys Ser Gln
 1250 1255 1260

Leu Gln Gln Cys Cys Leu Thr Leu Arg Thr Glu Gly Lys Glu Pro Asp
 1265 1270 1275 1280

Ile Pro Leu Tyr Lys Thr Leu Gln Thr Val Gly Pro Ser His Ala Arg
 1285 1290 1295

Thr Tyr Thr Val Ala Val Tyr Phe Lys Gly Glu Arg Ile Gly Cys Gly
 1300 1305 1310

Lys Gly Pro Ser Ile Gln Gln Ala Glu Met Gly Ala Ala Met Asp Ala
 1315 1320 1325

Leu Glu Lys Tyr Asn Phe Pro Gln Met Ala His Gln Lys Arg Phe Ile
 1330 1335 1340

Gly Arg Lys Tyr Arg Gln Glu Leu Lys Glu Met Arg Trp Glu Arg Glu
 1345 1350 1355 1360

His Gln Glu Arg Glu Pro Asp Glu Thr Glu Asp Ile Lys Lys
 1365 1370

<210> 3
 <211> 412
 <212> PRT
 <213> Caenorhabditis elegans

<400> 3

Met Ser Leu Phe Asn Ile Met Lys Gly Thr Ser Gly Gly Glu Pro Ile
 1 5 10 15

Leu His Asn Glu Arg Leu Glu Tyr Leu Gly Asp Ala Val Val Glu Leu
 20 25 30

Ile Val Ser His His Leu Tyr Phe Met Leu Thr His His Phe Glu Gly
 35 40 45

Gly Leu Ala Thr Tyr Arg Thr Ala Leu Val Gln Asn Arg Asn Leu Ala
 50 55 60

Thr Leu Ala Lys Asn Cys Arg Ile Asp Glu Met Leu Gln Tyr Ser His
 65 70 75 80

Gly Ala Asp Leu Ile Asn Val Ala Glu Phe Lys His Ala Leu Ala Asn
 85 90 95

Ala Phe Glu Ala Val Met Ala Ala Ile Tyr Leu Asp Gly Gly Leu Ala
 100 105 110

Pro Cys Asp Val Ile Phe Ser Lys Ala Met Tyr Gly His Gln Pro Val
115 120 125

Leu Lys Glu Lys Trp Asp His Ile Asn Glu His Glu Leu Lys Arg Glu
130 135 140

Asp Pro Gln Gly Asp Arg Asp Leu Ser Phe Ile Thr Pro Thr Leu Ser
145 150 155 160

Thr Phe His Ala Leu Glu Glu Arg Leu Gly Ile Gln Phe Asn Asn Ile
165 170 175

Arg Leu Leu Ala Lys Ala Phe Thr Arg Arg Asn Ile Pro Asn Asn Asp
180 185 190

Leu Thr Lys Gly His Asn Gln Arg Leu Glu Trp Leu Gly Asp Ser Val
195 200 205

Leu Gln Leu Ile Val Ser Asp Phe Leu Tyr Arg Arg Phe Pro Tyr His
210 215 220

His Glu Gly His Met Ser Leu Leu Arg Thr Ser Leu Val Ser Asn Gln
225 230 235 240

Thr Gln Ala Val Val Cys Asp Asp Leu Gly Phe Thr Glu Phe Val Ile
245 250 255

Lys Ala Pro Tyr Lys Thr Pro Glu Leu Lys Leu Lys Asp Lys Ala Asp
260 265 270

Leu Val Glu Ala Phe Ile Gly Ala Leu Tyr Val Asp Arg Gly Ile Glu
275 280 285

His Cys Arg Ala Phe Ile Arg Ile Val Phe Cys Pro Arg Leu Lys His
290 295 300

Phe Ile Glu Ser Glu Lys Trp Asn Asp Ala Lys Ser His Leu Gln Gln
305 310 315 320

Trp Cys Leu Ala Met Arg Asp Pro Ser Ser Ser Glu Pro Asp Met Pro
325 330 335

Glu Tyr Arg Val Leu Gly Ile Glu Gly Pro Thr Asn Asn Arg Ile Phe
340 345 350

Lys Ile Ala Val Tyr Tyr Lys Gly Lys Arg Leu Ala Ser Ala Ala Glu
355 360 365

Ser Asn Val His Lys Ala Glu Leu Arg Val Ala Glu Leu Ala Leu Ala
370 375 380

Asn Leu Glu Ser Met Ser Phe Ser Lys Met Lys Ala Lys Asn Asn Ser
385 390 395 400

Asn Met Arg Arg Arg Leu Glu Gln Asp Thr Ser Asp
405 410

<210> 4<211> 366<212> PRT<213> Saccharomyces pombe<400> 4

Met Gly Arg Phe Lys Arg His His Glu Gly Asp Ser Asp Ser Ser Ser
1 5 10 15

Ser Ala Ser Asp Ser Leu Ser Arg Gly Arg Arg Ser Leu Gly His Lys
20 25 30

Arg Ser Ser His Ile Lys Asn Arg Gln Tyr Tyr Ile Leu Glu Lys Lys
35 40 45

Ile Arg Lys Leu Met Phe Ala Met Lys Ala Leu Leu Glu Glu Thr Lys
50 55 60

His Ser Thr Lys Asp Asp Val Asn Leu Val Ile Pro Gly Ser Thr Trp
65 70 75 80

Ser His Ile Glu Gly Val Tyr Glu Met Leu Lys Ser Arg His Asp Arg
85 90 95

Gln Asn Glu Pro Val Ile Glu Glu Pro Ser Ser His Pro Lys Asn Gln
100 105 110

Lys Asn Gln Glu Asn Asn Glu Pro Thr Ser Glu Glu Phe Glu Glu Gly
115 120 125

Glu Tyr Pro Pro Pro Leu Pro Pro Leu Arg Ser Glu Lys Leu Lys Glu
130 135 140

Gln Val Phe Met His Ile Ser Arg Ala Tyr Glu Ile Tyr Pro Asn Gln
 145 150 155 160

Ser Asn Pro Asn Glu Leu Leu Asp Ile His Asn Glu Arg Leu Glu Phe
 165 170 175

Leu Gly Asp Ser Phe Phe Asn Leu Phe Thr Thr Arg Ile Ile Phe Ser
 180 185 190

Lys Phe Pro Gln Met Asp Glu Gly Ser Leu Ser Lys Leu Arg Ala Lys
 195 200 205

Phe Val Gly Asn Glu Ser Ala Asp Lys Phe Ala Arg Leu Tyr Gly Phe
 210 215 220

Asp Lys Thr Leu Val Leu Ser Tyr Ser Ala Glu Lys Asp Gln Leu Arg
 225 230 235 240

Lys Ser Gln Lys Val Ile Ala Asp Thr Phe Glu Ala Tyr Leu Gly Ala
 245 250 255

Leu Ile Leu Asp Gly Gln Glu Glu Thr Ala Phe Gln Trp Val Ser Arg
 260 265 270

Leu Leu Gln Pro Lys Ile Ala Asn Ile Thr Val Gln Arg Pro Ile Asp
 275 280 285

Lys Leu Ala Lys Ser Lys Leu Phe His Lys Tyr Ser Thr Leu Gly His
 290 295 300

Ile Glu Tyr Arg Trp Pro Ala Cys Val Asp Gly Ala Gly Gly Ser Ala
 305 310 315 320

Glu Gly Tyr Val Ile Ala Cys Ile Phe Asn Gly Lys Glu Val Ala Arg
 325 330 335

Ala Trp Gly Ala Asn Gln Lys Asp Ala Gly Ser Arg Ala Ala Met Gln
 340 345 350

Ala Leu Glu Val Leu Ala Lys Asp Tyr Ser Lys Phe Ala Arg
 355 360 365

<210> 5
 <211> 471
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 5

Met Gly Ser Lys Val Ala Gly Lys Lys Lys Thr Gln Asn Asp Asn Lys
 1 5 10 15

Leu Asp Asn Glu Asn Gly Ser Gln Gln Arg Glu Asn Ile Asn Thr Lys
 20 25 30

Thr Leu Leu Lys Gly Asn Leu Lys Ile Ser Asn Tyr Lys Tyr Leu Glu
 35 40 45

Val Ile Gln Leu Glu His Ala Val Thr Lys Leu Val Glu Ser Tyr Asn
 50 55 60

Lys Ile Ile Glu Leu Ser Pro Asn Leu Val Ala Tyr Asn Glu Ala Val
 65 70 75 80

Asn Asn Gln Asp Arg Val Pro Val Gln Ile Leu Pro Ser Leu Ser Arg
 85 90 95

Tyr Gln Leu Lys Leu Ala Ala Glu Leu Lys Thr Leu His Asp Leu Lys
 100 105 110

Lys Asp Ala Ile Leu Thr Glu Ile Thr Asp Tyr Glu Asn Glu Phe Asp
 115 120 125

Thr Glu Gln Lys Gln Pro Ile Leu Gln Glu Ile Ser Lys Ala Asp Met
 130 135 140

Glu Lys Leu Glu Lys Leu Glu Gln Val Lys Arg Glu Lys Arg Glu Lys
 145 150 155 160

Ile Asp Val Asn Val Tyr Glu Asn Leu Asn Glu Lys Glu Asp Glu Glu
 165 170 175

Glu Asp Glu Gly Glu Asp Ser Tyr Asp Pro Thr Lys Ala Gly Asp Ile
 180 185 190

Val Lys Ala Thr Lys Trp Pro Pro Lys Leu Pro Glu Ile Gln Asp Leu
 195 200 205

Ala Ile Arg Ala Arg Val Phe Ile His Lys Ser Thr Ile Lys Asp Lys
 210 215 220

Val Tyr Leu Ser Gly Ser Glu Met Ile Asn Ala His Asn Glu Arg Leu
 225 230 235 240

Glu Phe Leu Gly Asp Ser Ile Leu Asn Ser Val Met Thr Leu Ile Ile
 245 250 255

Tyr Asn Lys Phe Pro Asp Tyr Ser Glu Gly Gln Leu Ser Thr Leu Arg
 260 265 270

Met Asn Leu Val Ser Asn Glu Gln Ile Lys Gln Trp Ser Ile Met Tyr
 275 280 285

Asn Phe His Glu Lys Leu Lys Thr Asn Phe Asp Leu Lys Asp Glu Asn
 290 295 300

Ser Asn Phe Gln Asn Gly Lys Leu Lys Leu Tyr Ala Asp Val Phe Glu
 305 310 315 320

Ala Tyr Ile Gly Gly Leu Met Glu Asp Asp Pro Arg Asn Asn Leu Pro
 325 330 335

Lys Ile Arg Lys Trp Leu Arg Lys Leu Ala Lys Pro Val Ile Glu Glu
 340 345 350

Ala Thr Arg Asn Gln Val Ala Leu Glu Lys Thr Asp Lys Leu Asp Met
 355 360 365

Asn Ala Lys Arg Gln Leu Tyr Ser Leu Ile Gly Tyr Ala Ser Leu Arg
 370 375 380

Leu His Tyr Val Thr Val Lys Lys Pro Thr Ala Val Asp Pro Asn Ser
 385 390 395 400

Ile Val Glu Cys Arg Val Gly Asp Gly Thr Val Leu Gly Thr Gly Val
 405 410 415

Gly Arg Asn Ile Lys Ile Ala Gly Ile Arg Ala Ala Glu Asn Ala Leu
 420 425 430

Arg Asp Lys Lys Met Leu Asp Phe Tyr Ala Lys Gln Arg Ala Ala Ile
435 440 445

Pro Arg Ser Glu Ser Val Leu Lys Asp Pro Ser Gln Lys Asn Lys Lys
450 455 460

Arg Lys Phe Ser Asp Thr Ser
465 470

<210> 6
<211> 226
<212> PRT
<213> Escherichia coli

<400> 6

Met Asn Pro Ile Val Ile Asn Arg Leu Gln Arg Lys Leu Gly Tyr Thr
1 5 10 15

Phe Asn His Gln Glu Leu Leu Gln Gln Ala Leu Thr His Arg Ser Ala
20 25 30

Ser Ser Lys His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser Ile Leu
35 40 45

Ser Tyr Val Ile Ala Asn Ala Leu Tyr His Arg Phe Pro Arg Val Asp
50 55 60

Glu Gly Asp Met Ser Arg Met Arg Ala Thr Leu Val Arg Gly Asn Thr
65 70 75 80

Leu Ala Glu Leu Ala Arg Glu Phe Glu Leu Gly Glu Cys Leu Arg Leu
85 90 95

Gly Pro Gly Glu Leu Lys Ser Gly Gly Phe Arg Arg Glu Ser Ile Leu
100 105 110

Ala Asp Thr Val Glu Ala Leu Ile Gly Gly Val Phe Leu Asp Ser Asp
115 120 125

Ile Gln Thr Val Glu Lys Leu Ile Leu Asn Trp Tyr Gln Thr Arg Leu
130 135 140

Asp Glu Ile Ser Pro Gly Asp Lys Gln Lys Asp Pro Lys Thr Arg Leu

145

150

155

160

Gln Glu Tyr Leu Gln Gly Arg His Leu Pro Leu Pro Thr Tyr Leu Val
 165 170 175

Val Gln Val Arg Gly Glu Ala His Asp Gln Glu Phe Thr Ile His Cys
 180 185 190

Gln Val Ser Gly Leu Ser Glu Pro Val Val Gly Thr Gly Ser Ser Arg
 195 200 205

Arg Lys Ala Glu Gln Ala Ala Ala Glu Gln Ala Leu Lys Lys Leu Glu
 210 215 220

Leu Glu
 225

<210> 7
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 7

His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser
 1 5 10

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 8
 atccctttct tccgcatgtg

20

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 9
 gcccaaggcgt gacatgatat

20

<210> 10

<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 10
cggatcatta aagagcaagc

20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 11
tattcaccaa agagcttcgc

20

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 12
caatcgtgga aagaagcaga

20

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 13
gctcccattt ccgcttgctg

20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 14
atgctctctt tcccacctca

20

<210> 15
<211> 20
<212> DNA

<213> Artificial Sequence
<220>
<223> Synthetic

<400> 15
aaataactcca cacttgcatg

20

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 16
tgcacattca ccaaagtcaa

20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 17
agtctagggt cacaatctgg

20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 18
ttcagttgta gtggtccgac

20

<210> 19
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 19
caaggcacgc ctctcagatc gctagagaag gcttttctca

40

<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence
<220>

<223> Synthetic

<400> 20
cattaattct cgcagctagc gctgcgttct tcatcgacgc

40

<210> 21
<211> 35
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 21
ccaaatactg atcgacaact tattgaaact tctcc

35

<210> 22
<211> 37
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 22
gagtttgaag aagcaattgg agtaattttt actcatg

37

<210> 23
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 23
tcgacttctg gcaaggcat tcacatt

27

<210> 24
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 24
cctctgtgcc agcttctgtt tgtcag

26

<210> 25
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 25
tgtcagtttg tttgactttg ggacta

26

<210> 26
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 26
tttgctagga ggtggcgaag tttcac

26

<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 27
gcttgatggc ctcttctcca ggataaatgc

30

<210> 28
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 28
aatgctgtgc ctaattcctg tgcgtcttgc

30

<210> 29
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 29
caggtgctgt cctcatcaga ctcacactcg gattcactgg aactctct

48

<210> 30
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 30
cactgggcag gaaagaacta gggttg

26

<210> 31
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 31
 tggaaactat taaaactggg aggtgg

26

<210> 32
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 32
 aggcattggag ggagggggca tcatgaagg gaaagtgcct tgtccaggag

50

<210> 33
 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 33
 caaggcacgc ctctcagatc gctagagaag gcttttctca

40

<210> 34
 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 34
 cattaattct cgcagctagc gctgcgttct tcatcgacgc

40

<210> 35
 <211> 20
 <212> PRT
 <213> Homo sapiens
 <400> 35

Cys	Arg	Ser	Asp	Tyr	Asp	Arg	Gly	Arg	Thr	Pro	Ser	Arg	His	Arg	Ser
1				5					10					15	

Tyr Glu Arg Ser

20

<210> 36
<211> 20
<212> PRT
<213> Homo sapiens
<400> 36

Cys Arg Trp Glu Arg Glu His Gln Glu Arg Glu Pro Asp Glu Thr Glu
1 5 10 15

Asp Ile Lys Lys
20

<210> 37
<211> 466
<212> PRT
<213> Homo sapiens

<400> 37

Asn Pro Asp His Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln
1 5 10 15

Pro Lys Tyr Gly Asp Arg Lys Val His His Met His Met Arg Lys Lys
20 25 30

Gly Ile Asn Thr Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp
35 40 45

Pro Thr Pro Ser Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly
50 55 60

Asp Ala Val Val Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe
65 70 75 80

Pro Ser Leu Glu Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val
85 90 95

Gln Asn Gln His Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro
100 105 110

Phe Met Leu Tyr Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu
115 120 125

Arg His Ala Met Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr
130 135 140

Leu Glu Gly Ser Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu
145 150 155 160

Phe Asn Asp Pro Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His
165 170 175

Pro Leu Gln Leu Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr
180 185 190

Ser Pro Val Leu Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val
195 200 205

Ile Phe Thr His Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr
210 215 220

Val Gly Phe Asn His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe
225 230 235 240

Leu Gly Asp Ser Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile
245 250 255

His Phe Pro Asp His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser
260 265 270

Leu Val Asn Asn Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met
275 280 285

Gln Glu Tyr Ala Ile Thr Asn Asp Lys Thr Lys Arg Pro Val Gly Leu
290 295 300

Arg Thr Lys Thr Leu Ala Asp Leu Leu Glu Ser Phe Ile Ala Ala Leu
305 310 315 320

Tyr Thr Asp Lys Asp Leu Glu Tyr Val His Thr Phe Met Asn Val Cys
325 330 335

Phe Phe Pro Arg Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Asp
340 345 350

Pro Lys Ser Gln Leu Gln Gln Cys Cys Leu Thr Leu Arg Thr Glu Gly
355 360 365

Lys Glu Pro Asp Ile Pro Leu Tyr Lys Thr Leu Gln Thr Val Gly Pro
370 375 380

Ser His Ala Arg Thr Tyr Thr Val Ala Val Tyr Phe Lys Gly Glu Arg
385 390 395 400

Ile Gly Cys Gly Lys Gly Pro Ser Ile Gln Gln Ala Glu Met Gly Ala
405 410 415

Ala Met Asp Ala Leu Glu Lys Tyr Asn Phe Pro Gln Met Ala His Gln
420 425 430

Lys Arg Phe Ile Gly Arg Lys Tyr Arg Gln Glu Leu Lys Glu Met Arg
435 440 445

Trp Glu Arg Glu His Gln Glu Arg Glu Pro Asp Glu Thr Glu Asp Ile
450 455 460

Lys Lys
465